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(54) Title: A PROTEIN FAMILY RELATED TO IMMEDIATE-EARLY PROTEIN EXPRESSED BY HUMAN ENDOTHELIAL CELLS DURING DIFFERENTIATION (57) Abstract This invention provides a novel family of tissue specific genes and proteins that are related to a G-protein-coupled receptor gene and the receptor protein. The gene is an intermediate early gene that is expressed in differentiating endothelial cells. In particular, this invention provides a gene, <i>edg-1</i> , that is an immediate-early gene that encodes a G-protein-coupled receptor in endothelial cells. This invention also provides the G-protein-coupled receptor protein that is encoded by <i>edg-1</i> .		

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A PROTEIN FAMILY RELATED TO IMMEDIATE-EARLY PROTEIN EXPRESSED
BY HUMAN ENDOTHELIAL CELLS DURING DIFFERENTIATION

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3

4 BACKGROUND OF INVENTION

5 The endothelium is composed of a monolayer of quiescent
6 cells, endothelial cells. Endothelial cells, which form the
7 inner lining of blood vessels participate in a multiplicity
8 of physiological functions, including the formation of a
9 selective barrier for the translocation of blood constituents
10 and macromolecules to underlying tissues and the maintenance
11 of a non-thrombogenic interface between blood and tissue.
12 Endothelial cells are also an important component in the
13 development of new capillaries and blood vessels. Blood
14 vessel development, which is called angiogenesis, occurs
15 during developmental periods, such as during development of
16 the vascular system, and as part of the pathophysiology of a
17 variety of disease states, such as psoriasis, arthritis,
18 chronic inflammatory conditions, diabetic retinopathy, and
19 tumor development.

20 Angiogenesis, which involves the organized migration,
21 proliferation, and differentiation of the endothelial cells,
22 is initiated by the endothelial cell in response to angiogenic
23 stimuli and can be separated into three distinct events: cell
24 migration, cell proliferation and cell differentiation,
25 whereby the cells organize into a tubular structure.

26 These events are mediated in vitro, and most likely in
27 vivo, by mitogenic polypeptides. The migration of endothelial
28 cells is induced by factors, including the heparin binding

1 growth factors and angiotropin. Proliferation is induced by
2 the heparin binding growth factors (hereinafter HBGFs) and
3 differentiation and cellular organization is induced by
4 polypeptides, including interleukin-1 (hereinafter IL-1),
5 tumor necrosis factor (hereinafter TNF), gamma-interferon,
6 transforming growth factor alpha and beta (hereinafter TGF- α
7 and TGF- β , respectively) and phorbol myristic acetate
8 (hereinafter PMA).

9 The extracellular matrix (hereinafter ECM), which
10 contains numerous components, also modulates endothelial cell
11 differentiation. If endothelial cells are cultured in vitro
12 on collagen gels in the presence of PMA organized networks of
13 tubular structures form, and, if the cells are cultured in ECM
14 conditioned medium the formation of tubular structures is
15 accelerated.

16 The importance of the ECM components for mediation of
17 endothelial cell differentiation is evidenced by the
18 observations that antibodies that have been prepared against
19 fibronectin and laminin inhibit formation of the
20 differentiated phenotype, while proteolytic modification of
21 fibronectin by plasmin leads to rapid modification of the
22 endothelial cell phenotypic changes that are observed in
23 vitro. In addition, competitive inhibitors of the laminin
24 and fibronectin receptor binding domains also inhibit the
25 ability of endothelial cells to complete the non-terminal
26 differentiation program.

27 As discussed above, the polypeptide cytokines and PMA
28 inhibit the HBGF-1-induced proliferation of endothelial cells
29 and induce differentiation thereof. These factors induce a
30 reversible phenotypic transition from a non-polar cobblestone
31 monolayer into a polar elongated, fibroblast-like phenotype.
32 The inhibition of HBGF-1-induced proliferation is mediated,
33 at least in part, via down regulation of the HBGF-1 receptor.

1 It is also known that PMA activates protein kinase C,
2 which a family of phospholipid- and calcium-activated protein
3 kinases. This activation results in the transcription of an
4 array of proto-oncogene transcription factors, including c-
5 fos, c-myc and c-jun, proteases, protease inhibitors,
6 including collagenase type I and plasminogen activator
7 inhibitor, and adhesion molecules, including intercellular
8 adhesion molecule I. Protein kinase C activation antagonizes
9 growth factor activity by the rapid phosphorylation of the
10 epidermal growth factor receptor. Phosphorylation decreases
11 tyrosine kinase activity.

12 Upon induction of differentiation of endothelial cells
13 in vitro by a cytokine or PMA, a set of immediate-early genes
14 are rapidly induced via a pathway that does not require
15 protein synthesis. Included among these immediate-early genes
16 are transcriptional factors, cytokines, cytoskeletal proteins,
17 nuclear hormone receptors and extracellular matrix receptors.

18 Cell surface receptors bind circulating signal
19 polypeptides, such as growth factors and hormones, as the
20 initiating step in the induction of numerous intracellular
21 effector functions. Receptors are classified on the basis of
22 the particular type of pathway that is induced. Included
23 among these classes of receptors are those that bind growth
24 factors and have intrinsic tyrosine kinase activity, such as
25 the HBGF receptors and those that couple to effector proteins
26 through guanine nucleotide binding regulatory proteins,
27 hereinafter referred to as G-protein coupled receptors and G-
28 proteins, respectively. The G-protein transmembrane signaling
29 pathways consist of three proteins: receptors, G proteins and
30 effectors.

31 G proteins, which are the intermediaries in transmembrane
32 signaling pathways, are heterodimers and consist of α , β and
33 gamma subunits. Among the members of a family of G proteins

1 the α subunits differ. Functions of G proteins are regulated
2 by the cyclic association of GTP with the α subunit followed
3 by hydrolysis of GTP to GDP and dissociation of GDP.

4 G-protein coupled receptors are a diverse class of
5 receptors that mediate signal transduction by binding to G-
6 proteins. Signal transduction is initiated via ligand binding
7 to the cell membrane receptor, which stimulates binding of the
8 receptor to the G-protein. The receptor-G-protein interaction
9 releases GDP, which is specifically bound to the G-protein,
10 and permits the binding of GTP, which activates the G-protein.
11 Activated G-protein dissociates from the receptor and
12 activates the effector protein, which regulates the
13 intracellular levels of specific second messengers. Examples
14 of such effector proteins include adenylyl cyclase, guanylyl
15 cyclase, phospholipase C, and others.

16 G-protein-coupled receptors, which are glycoproteins, are
17 known to share certain structural similarities and homologies
18 (see, e.g., Gilman, A.G., Ann. Rev. Biochem. 56: 615-649
19 (1987), Strader, C.D. et al. The FASEB Journal 3: 1825-1832
20 (1989), Kobilka, B.K., et al. Nature 329: 75-79 (1985) and
21 Young et al. Cell 45: 711-719 (1986)). Among the G-protein-
22 coupled receptors that have been identified and cloned are the
23 substance K receptor, the angiotensin receptor, the α - and β -
24 adrenergic receptors and the serotonin receptors. G-protein-
25 coupled receptors share a conserved structural motif. The
26 general and common structural features of the G-protein-
27 coupled receptors are the existence of seven hydrophobic
28 stretches of about 20-25 amino acids each surrounded by eight
29 hydrophilic regions of variable length. It has been
30 postulated that each of the seven hydrophobic regions forms
31 a transmembrane α helix and the intervening hydrophilic
32 regions form alternately intracellularly and extracellularly

1 exposed loops. The third cytosolic loop between transmembrane
2 domains five and six is the intracellular domain responsible
3 for the interaction with G-protein.

4 G-protein-coupled receptors are known to be inducible.
5 This inducibility was originally described in lower
6 eukaryotes. For example, the cAMP receptor of the cellular
7 slime mold, Dictyostelium, is induced during differentiation
8 (Klein et al., Science 241: 1467-1472 (1988)). During the
9 Dictyostelium discoideum differentiation pathway, cAMP,
10 induces high level expression of its G-protein-coupled
11 receptor. This receptor transduces the signal to induce the
12 expression of the other genes involved in chemotaxis, which
13 permits multicellular aggregates to align, organize and form
14 stalks (see, Firtel, R.A., et al. Cell 58: 235-239 (1989) and
15 Devreotes, P., Science 245: 1054-1058 (1989)). H u m a n
16 endothelial cells utilize a series of morphological correlates
17 during its differentiation pathway, discussed supra, in which
18 individual cells migrate, align and organize to form
19 multicellular capillary-like structures.

20 SUMMARY OF THE INVENTION

21 It is one object of this invention to provide a novel G-
22 protein-coupled receptor that is the product of an immediate
23 early gene that is expressed in endothelial cells during the
24 early stage of differentiation.

25 It is another object of this invention to provide a
26 family of proteins that are expressed in a tissue-specific
27 manner and that are related to the novel G-protein-coupled
28 receptor that is the product of an immediate early gene that
29 is expressed in endothelial cells during the early stage of
30 differentiation.

1 It is another object of this invention to provide DNA
2 molecules that encode each member of the family of proteins
3 that are expressed in a tissue-specific manner and that are
4 related to the novel G-protein-coupled receptor that is the
5 product of an immediate early gene that is expressed in
6 endothelial cells during the early stage of differentiation.

7 It is another object of this invention to provide DNA
8 molecules that encode the novel G-protein-coupled receptor
9 that is the product of an immediate early gene that is
10 expressed in endothelial cells during the early stage of
11 differentiation.

12 In accordance with this invention there is provided a DNA
13 molecule that encodes edg-1 gene product, which is the product
14 of an immediate-early gene that is expressed in the early
15 stage of differentiation of endothelial cells in response to
16 PMA or IL-1.

17 This invention provides a gene and protein, which is the
18 first immediate-early gene that encodes a G-protein-coupled
19 receptor.

20 Unless defined otherwise, all technical and scientific
21 terms used herein have the same meaning as is commonly
22 understood by one of ordinary skill in the art to which this
23 invention belongs. Although methods and materials similar or
24 equivalent to those described herein can be used in the
25 practice of testing of the present invention, the preferred
26 methods and materials are now described. All publications
27 mentioned hereunder are incorporated by reference.

1 BRIEF DESCRIPTION OF THE FIGURES

2 Figure 1. The identification of edg-1, an Immediate
3 early gene induced by PMA in HUVEC (human umbilical vein
4 endothelial cells).

5 Confluent cultures of HUVEC were treated with 20 ng/ml
6 of PMA for the indicated times. The cells were then lysed,
7 RNA purified, and total RNA (10 µg) analyzed by Northern blot
8 analysis. The cDNA probes that were used were edg-1 (A) and
9 glyceraldehyde-3-phosphate (GAPDH) (B) cDNA.

10 Figure 2. Confluent cultures of HUVEC were treated with
11 the indicated reagents for 4 hour and the RNA was isolated.
12 Total RNA (10 µg) was fractionated by 1% agarose-formaldehyde
13 gel electrophoresis, blotted onto a zeta-probe membrane and
14 hybridized with [³²P]-labeled edg-1 (A) or a GAPDH (B) cDNA
15 probes. The following reagents were used: PMA (20 ng/ml), chx
16 (5 µg/ml), Actinomycin D (Act D) (2 µg/ml). Each reagent was
17 used either alone or in combination.

18 Figure 3. Confluent cultures of HUVEC were pre-treated
19 with 20 ng/ml PMA for 4 hour. Either Act D (2 µg/) alone or
20 with chx (5 µg/ml) was added to the cultures, at a time
21 designated 0. At the indicated time points, cultures were
22 harvested and Northern blot analysis was performed on total
23 RNA as described above using the edg-1 (A) and GAPDH (B) cDNA
24 probes.

25 Figure 4. HUVEC were either untreated or treated with
26 20 ng/ml PMA for 2 hour after which nuclei were prepared.
27 Run-off transcripts were obtained by labelling 10⁷ nuclei in
28 vitro with [³²P]-UTP. RNA was purified and hybridized to
29 immobilized plasmid DNA encoding edg-1 (10 µg/slot), human
30 fibronectin (fn) (2 µg/slot) and pBluescript (pBS) (10
31 µg/slot).

1 Figure 5. Nucleotide and Deduced Amino Acid Sequence of
2 Human edg-1.

3 The nucleotide (1-2774) and deduced amino acid sequence
4 (1-380) is shown for human edg-1 cDNA. The deduced
5 transmembrane domains are underline and potential N-linked
6 glycosylation sites are shown with ann asterisk. Possible
7 serine and threonine phosphorylation sites are shown with
8 closed circles. The basic amino acid-rich intracellular
9 domain, which is located between transmembrane domains five
10 and six is highlighted with open circles. The Kozak consensus
11 translation initiation sequence (5') and polyadenylation sites
12 (3') are shown with double lines underneath their respective
13 sequences. The Genbank accession number for this nucleotide
14 sequence is M31210.

15 Figure 6. The amino acid sequence of the putative edg-
16 1 translation product was aligned with Substance K receptor
17 (SKR), Substance P receptor (SPR), β_2 -adrenergic receptor
18 (B2AR), Serotonin receptor 1c (5HTC), α_2 -adrenergic receptor
19 (A2A), Serotonin receptor 1a (5HT1a), Rhodopsin (OSPD) and
20 angiotensin receptor (MAS). Highly homologous regions are
21 boxed and indicated on the linear schematic.

22 Figure 7. A structural model for the putative edg-1
23 translation product is shown. This model is analogous to other
24 G-protein-coupled receptors. The potential N-linked
25 glycosylation sites are indicated with an inverted "Y".
26 Potential phosphorylation sites at serine and threonine
27 residues are shown with dark circles. The third cytosolic
28 intracellular domain, which is between transmembrane domains
29 5 and 6 contains a highly basic region (11/35 residues) is
30 also indicated.

1 Figure 8. Hydrophobicity Profile of edg-1 Translation
2 Product. The deduced amino acid sequence of edg-1 was
3 analyzed for hydrophobic regions and the amino acid sequence
4 (residues) plotted against the hydrophobicity index. The
5 putative transmembrane (TM) domains are indicated.

6 Figure 9. Expression of edg-1 transcript in human cells.
7 Total RNA (5 µg) from human saphenous vein smooth muscle
8 cells (S), foreskin fibroblasts (F), HeLa cells (H),
9 epidermoid carcinoma (A431) cells (A), melanocytes (M), brain
10 tissue (B) and endothelial cells (E) were reverse transcribed
11 into cDNA and amplified with edg-1 specific oligonucleotide
12 primers that span the carboxy-terminal tail domain (A) and
13 the third cytosolic loop (B). Amplified DNA was separated
14 by agarose gel electrophoresis and visualized by ethidium
15 bromide staining. Molecular weight markers (indicated by
16 arrows) are from top to bottom: 1.6 Kb, 1.0 Kb, 0.5 Kb, 0.4
17 Kb, 0.3 Kb, 0.2 Kb and 0.15 Kb.

18 It can be seen in (A) that transcript of the expected
19 size, about 600 bp,, which was amplified using oligonucleotide
20 primers specific for the C-terminal domain, was present in
21 RNA from all the cultured cell lines and human brain. In
22 contrast, when the transcript was amplified using an a pair
23 oligonucleotides that span the third intracellular loop, cell
24 or tissue specific bands were observed.

25 DESCRIPTION OF THE PREFERRED EMBODIMENTS

26 In the invention described herein a novel gene, edg, and
27 the protein encoded thereby has been identified. In addition,
28 this invention provides a family of proteins that are
29 structurally and functionally related to this protein as well
30 as DNA molecules, but that are tissue or cell type specific
31 are provided.

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1 As used herein, the edg-G-protein-coupled receptor family
2 is a family of related proteins that share substantial
3 homology and structure and that contain common constant
4 regions or domains but differ in at least one variable region
5 or domain that includes the third cytosolic loop. See, e.g.,
6 Figures 6, 7, and 9. The particular variable region and,
7 thus, each family member, is expressed in a tissue-specific
8 manner.

9 As used herein, expression of a transcript in a tissue-
10 specific manner includes expression of transcripts that are
11 expressed in only certain tissues or cell types. Such tissue-
12 specific expression can be effected through a variety of
13 mechanisms, including the expression of different genes in
14 each tissue or cell type, through alternative splicing of the
15 same gene in each tissue or cell type, or through
16 recombination of germ line DNA in during development or
17 differentiation of each cell type.

18 As used herein, the edg-1-G-coupled protein receptor
19 transcript is the intermediate early transcript that is
20 expressed in the early stage of differentiation in endothelial
21 cells that can be induced or stimulated with PMA and
22 interleukin-1 (IL-1) but not with TGF- β , HBGF-1, or α -
23 thrombin. The edg-1 G-coupled protein receptor transcript
24 encodes the edg-1 G-coupled protein receptor.

25 As used herein, the edg-1-G-coupled protein receptor
26 transcript family is a family of transcripts that are
27 expressed in a tissue-specific manner and encode members of
28 the family of related proteins that share substantial homology
29 and structure and that contain common constant regions or
30 domains but differ in at least one variable region that
31 includes the third cytosolic loop.

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1 As used herein, DNA encoding a protein includes any DNA
2 molecule that encodes a protein that has substantially the
3 same amino acid sequence. Each of such proteins may, however,
4 differ at sites that are not essential to protein function and
5 includes proteins isolated from different individuals in the
6 same species, proteins isolated from different species that
7 share substantially the same biological activities, and
8 proteins isolated from different cultured cell lines.

9 As used herein, the edg-1 transcript refers to the 2.8
10 Kb (about 3 Kb) transcript that encodes the receptor protein.
11 This term is herein used interchangeably with the edg
12 transcript, edg mRNA. The edg-1 transcript also refers to this
13 transcript, but also refers to the 1-Kb clone that was
14 isolated from the differential screen, which contained a poly
15 A tract at 3' end, a unique nucleotide sequence and hybridized
16 to the about 3.0 Kb PMA inducible mRNA species, the edg-1
17 transcript.

18 Because PMA inhibits endothelial cell proliferation and
19 induces differentiation, the identification and isolation of
20 immediate-early genes yields insight into the molecular
21 mechanisms involved in the regulation of endothelial cell
22 differentiation.

23 Immediate-early genes that are expressed in endothelial
24 cells may be isolated from any source of endothelial RNA. In
25 one embodiment of this invention, human umbilical vein
26 endothelial cells (hereinafter HUVEC) are used. The HUVEC are
27 either untreated and treated with PMA, IL-2 or any other
28 signal that induces these genes.

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1 The desired immediate-early genes can be identified by
2 any means in which the transcripts comparing the transcripts
3 in cells that are stimulated with PMA, IL-2 or other inducer
4 with the transcripts that are present in untreated cells.
5 Those that are present only in the treated cells are, thus,
6 immediate-early genes. In addition, any member of the G-
7 protein-coupled receptor family of this invention can be
8 identified by screening an appropriate library with an
9 appropriate probe derived from the edg-1 clone. For example,
10 an appropriate probe would be one derived from the 3' end of
11 the clone. Any methods known to those of skill in the art to
12 accomplish this may be used.

13 In endothelial cells the immediate-early gene of this
14 invention is the edg-1 encoding gene. It is induced by IL-1,
15 LPS or PMA, but not by HBGF-1, TGF- β , or α -thrombin. The edg-
16 1 clone provided herein encodes a protein that shares many
17 structural and sequence similarities with known G-protein-
18 coupled receptors, including the β -adrenergic, substance K,
19 substance P, rhodopsin, serotonin (5-HT), tachykinin receptors
20 and the cAMP receptor of Dictyostelium.

21 The N-linked glycosylation site at Asn₃₀ is also found in
22 the Substance K and angiotensin receptors. The two N-linked
23 glycosylation sites are found within the amino-terminal domain
24 of all G-protein-coupled receptors. The region in proximity
25 to the second and third hydrophobic domains is highly
26 conserved among all such receptors, including that encoded by
27 edg-1. In the β_2 -adrenergic receptor Asp₁₃₀ is known to be
28 absolutely necessary for G-protein; in the edg-1-encoded
29 protein the Asp/Glu-Arg is conserved.

30 Although the overall sequence similarity between the
31 edg-1 G-protein-coupled receptor of this invention and other
32 such receptor is quite divergent, there is a significant
33 degree of sequence similarity within the carboxy-terminal

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1 half, particularly within transmembrane domain seven. It is
2 most similar to those receptors that recognize peptides as
3 receptor ligands.

4 The intracellular hydrophilic loop regions contain four
5 potential phosphorylation sites at residues Thr₇₂, Ser₂₃₁, Thr₂₃₅
6 and at Ser₃₅₁. This feature is common to many G-protein-
7 coupled receptors. Phosphorylation at the Ser and Thr
8 residues within the intracellular domains has been implicated
9 in the phenomenon of receptor desensitization.

10 The hydrophilic region between transmembrane domains five
11 and six is the region that is absolutely necessary for G-
12 protein coupling and it is highly divergent among members of
13 the G-protein-coupled receptor proteins. In the G-protein-
14 coupled receptor that is encoded by edg-1, this region is
15 highly basic. The family of edg-1 related tissue-specific
16 proteins provided in this invention differ in this region and,
17 thus, most likely differ in their respective binding or
18 coupling interactions with the G-protein or protein ligands.

19 The ligand that binds to each of the members of the
20 family of G-protein-coupled receptor proteins of this
21 invention can be identified by methods that are known to those
22 of skill in the art. For example, xenopus oocytes can be
23 transfected with DNA that encodes the particular protein. The
24 protein will be expressed on the cell surface of the oocytes.
25 Since these oocytes are sensitive to calcium exchange across
26 the cell membrane, binding of the appropriate ligand causes
27 calcium exchange across membrane. Labeled calcium can be used
28 and the ligand that causes labeled calcium exchange can be
29 identified. Among the candidates for the ligand that binds
30 to the edg-1-G-protein coupled receptor are ATP, AMP,
31 adenosine, leukotrienes, prostenoids, histamine, bombasin,
32 thrombin, azopressin, bradykinin, endothelin, serotensin,
33 substance P and neuropeptide.

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1 The following examples are included for illustrative
2 purposes only and are not intended to limit the scope of the
3 invention.

4 EXAMPLE 1

5 Materials and Cell Culture

6 Recombinant human interleukin α (IL- 1α), which was the
7 gift of Dr. Peter Lomedico, Hoffman La Roche, Nutley, NJ.
8 Recombinant human HBGF- 1α was obtained from Anthony Jackson,
9 American Red Cross, Rockville, MD. Porcine TGF- β was purchased
10 from R & D Systems.

11 Primary cultures of human umbilical vein endothelial
12 cells (HUVEC) were obtained from Dr. Michael Gimbrone, Harvard
13 Medical School, Boston, MA, and were grown on fibronectin-
14 coated plates in Medium 199 supplemented with 10% (v/v) fetal
15 bovine serum, 1x antibiotic and antimycotic mixture (GIBCO,
16 Grand Island, NY), 150 μ g/ml crude endothelial cell growth
17 factor (Maciag et al., 1981) and 5 U/ml heparin (Sigma) as
18 described in Maciag et al. ((1981) J. Biol. Chem. 91, 420-
19 426). Cells were subcultured at a 1:5 split ratio and
20 cultures between passages of 4 and 12 were used. At
21 confluence, cells were maintained in medium without the growth
22 factor and heparin for two days to achieve quiescence.

23 RNA Preparation and cDNA Library Construction

24 Total RNA was obtained from cells that either untreated
25 or treated with 20 ng/ml PMA (Sigma) and 5 μ g/ml of
26 cycloheximide (hereinafter chx) (Sigma) for 4 hours. The
27 cells were rinsed with phosphate-buffered saline, lysed in 4M
28 guanidinium isothiocyanate and total RNA purified as described
29 in Winkles, J., et al. ((1987) Proc. Natl. Acad. Sci. USA 84,

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1 7124-7128). Poly A⁺ RNA (10 µg) from HUVEC exposed to PMA
2 and chx was converted to double-stranded cDNA and cloned into
3 the Eco RI site of lambda gt10, using the cDNA synthesis kit
4 from Bethesda Research Labs (Gaithersburg, MD) and the cDNA
5 cloning kit from Amersham (Chicago, IL). The library contained
6 > 10⁶ independent clones, with an average insert size of
7 approximately 1 Kb.

8 Northern Blot Analysis.

9 Total RNA (10 µg) was electrophoresed on a 1% agarose
10 gel containing 2.2 M formaldehyde, capillary-blotted onto
11 Zeta-probe membrane (Biorad) and UV cross-linked (Maniatis et
12 al. (1982) In Molecular Cloning: A Laboratory Manual, Cold
13 Spring Harbor Laboratory, Cold Spring Harbor, NY). The cDNA
14 insert fragment for edg-1 (2.8 Kb) or human GAPDH (1 Kb) was
15 labeled to high specific activity (>10⁸ cpm/µg) using a random
16 primer labeling kit (BRL) and was used to hybridize filters
17 in Church-Gilbert buffer (0.5 M sodium phosphate pH 7.2,
18 containing 7% SDS and 1% bovine serum albumin, 1mM EDTA and
19 20% formamide at 65° C for 16-20 hrs. Filters were washed
20 twice for 15 min at high-stringency (0.1xSSC, 65° C).

21 Differential Screening of cDNA Library

22 The differential screen was performed by plating 2 x 10⁴
23 pfu of the library onto bacteriological plaques (15 cm
24 diameter) containing LB agar. The phage were allowed to grow
25 at 37° C until plaques were approximately 0.5 mm in diameter.
26 Phage DNA was adsorbed onto Gene-screen plus nylon filters
27 (Dupont, DE), in duplicate, denatured, neutralized, and UV
28 cross-linked.

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1 The probe for differential screening was prepared by
2 reverse transcription of 1 μ g of poly A⁺ RNA from control and
3 PMA/chx-treated HUVEC. The reaction conditions were as
4 follows: 50 mM Tris HCl, pH 8.3, 75 mM KCl, 20 mM
5 dithiothreitol, 3 mM MgCl₂, 500 μ Ci [³²P]- α -dCTP, 20 μ M dCTP,
6 200 μ M each of dATP, dCTP, and dTTP, 0.5 μ g/ml of oligo dT₁₂₋₁₈
7 and 400 units of MMLV-reverse transcriptase (Bethesda
8 Research Labs, Gaithersburg, MD).

9 After incubation at 37° C for 60 minutes, RNA was
10 hydrolyzed by treatment with 100 μ l 0.6M NaOH and 20 mM EDTA
11 for 30 minutes at 65° C. The cDNA was purified on Sephadex
12 G-50 columns and ethanol-precipitated. Duplicate filters were
13 incubated with 10 cpm/ml of cDNA for 48 hours at 65° C in
14 hybridization buffer containing 2% SDS, 1 M NaCl and 10%
15 dextran sulfate. The filters were washed twice for 30 min at
16 65° C with 2xSSC containing, 1% SDS followed by two additional
17 washes for 30 min at 65° C with 0.1xSSC containing 1% SDS.

18 The filters were autoradiographed and duplicates were
19 superimposed on each other to isolate PMA/chx-induced signals.
20 Differential signals were plaque-purified by repeating the
21 screening process. Insert cDNA was prepared and used for either
22 Northern blot analysis or subcloning into plasmid vectors.

23 Of the twelve positive signals obtained from >10⁵ pfu of
24 the library three were found to be consistently positive. Two
25 of the clones had inserts had sequences identical to the
26 sequence of DNA that encodes human collagenase Type 1. The
27 third clone, herein called edg-1 (1-Kb) contained a poly A
28 tract at 3' end, a unique nucleotide sequence and hybridized
29 to a 3.0 Kb PMA inducible mRNA species.

30 This 1 kb insert was used to rescreen two additional cDNA
31 libraries-lambda gt10 and cDM8. The largest clone was 2.8
32 kb. Further investigation and analysis was conducted using
33 this clone, which is expressed at high levels (0.05%) in the
34 HUVEC.

In order to determine the characteristics of the rapid edg-1 induction, Northern blot analysis was performed with HUVEC that had been treated for 4 hours with PMA and chx, alone or in combination (Figure 2). As can be seen in Figure 2, the 3.0 KB mRNA edg transcript was induced independently by PMA and chx, but was superinduced in the presence of both.

Chx was shown to exert the superinduction effect by stabilizing the *edg-1* transcript (Figure 3). HUVEC were stimulated for 4 hour with PMA and subsequently incubated with actinomycin D, in inhibitor of transcription both in the presence and absence of chx. As shown in Figure 3 steady-state levels of the *edg-1* mRNA declined to undetectable levels two hours after the addition of actinomycin D; whereas, chx prevented this decline.

In order to ascertain at what level PMA induces *edg-1* mRNA, *edg 1* induction in the presence of actinomycin D was investigated. As shown in Figure 2, actinomycin D repressed the inductive effect of PMA, which suggests that PMA induces the transcription of the *edg-1* gene.

EXAMPLE 5Nuclear Run-On Transcription.

Nuclei (10^7) were prepared from quiescent HUVEC untreated or treated with 20 ng/ml PMA for 2 hr. *In vitro* labeled, run-off transcripts were prepared by incubating the nuclei with 250 μ Ci of [α - 32 P]-UTP (.6000 CI/mmol, Amersham), 10mM ATP, CTP, GTP, in the reaction buffer containing 20mM Tris-HCl, pH 7.9, 140mM KCl, 10mM MgCl₂ and 1mM dithiothreitol as described (Nevins, J., (1987) Meth. Enzymol. 152, 234-240).

The labeled RNA was purified (Winkles, J., supra.) and hybridized to nylon filters containing either 10 μ g of denatured plasmid edg-1 cDNA, 2 μ g of human fibronectin or 10 μ g of pBluescript (Stratagene). The hybridization and washing conditions were identical to those described for the differential hybridization.

Nuclei were prepared from untreated HUVEC or from HUVEC treated with PMA for 2 hours. Labeled run-on transcripts were obtained and hybridized to immobilized plasmid DNA containing the edg-1 insert and to a control plasmid containing fibronectin-encoding DNA or to a Bluescript plasmid (Figure 4). Edg-1 transcription was significantly induced in nuclei from the PMA treated HUVEC.

EXAMPLE 6DNA Sequence Analysis.

The structure of the edg-1 gene and gene product was elucidated by DNA sequencing of the 2.8 Kb cDNA clone.

Plasmid DNA for edg-1 (2.8Kb) was obtained by screening a cDNA library from HUVEC constructed in the vector, cDM8, which was a gift of Brian See, Harvard Medical School) with the (1.6Kb) insert obtained from the cDNA library in lambda

1 gtl0, discussed in Example 1. Double-stranded sequence
2 analysis was performed using the sequenase-2 enzyme (USBC),
3 following the manufacturer's instructions. Successive
4 primers were synthesized and used to sequence both strands of
5 the cDNA clone. The DNA sequence was analyzed by the
6 Intelligenetics Sequence Analysis program.

7 As shown in Figure 5, the complete nucleotide sequence
8 of the edg-1 cDNA clone is 2774 bp long and, at nucleotide 251
9 from the 5' end, contains a consensus translation initiation
10 sequence, which is followed by an open-reading frame (ORF)
11 that encodes 380 amino acids. The ORF is followed by a 3',
12 A/T-rich, 1.3 Kb untranslated region followed by a poly A
13 tail. A/T rich sequence motifs in 3' untranslated regions have
14 been implicated in conferring rapid RNA degradation of
15 intermediate-early mRNAs. There are two consensus
16 polyadenylation sites (AATAAA) at nucleotides 2590 and 2737,
17 respectively. The edg-1 clone also contains about 250 bp of
18 5' untranslated region.

19 The deduced amino acid sequence contains a non-
20 hydrophobic amino-terminal stretch of 46 amino acids, which
21 contain two potential N-linked glycosylation sites at residues
22 29 and 35. This stretch is followed by seven alternating
23 stretches of hydrophobic regions, each about 20 amino acid
24 residues long. There are 8 hydrophilic regions. Each of the
25 hydrophobic regions is flanked by hydrophilic regions of 7 to
26 19 amino acids, except for the region between the fifth and
27 sixth transmembrane domain, which is 35 residues long and is
28 rich in basic and dibasic residues. The last transmembrane
29 domain is followed by a long, 66 amino acid, stretch of
30 hydrophilic residues that include an abundance of serine and
31 threonine residues.

EXAMPLE 7Reverse Transcriptase-Polymerase Chain Reaction Analysis

RNA from HUVEC was purified as described in Example 1. RNA from human saphenous vein smooth muscle cells, human foreskin fibroblasts, human epidermoid carcinoma cells (A431), human cervical carcinoma cells (HeLa), human melanocytes and total brain were the generous gift of Dr. Jeffrey Winkles of the American National Red Cross.

Total RNA (5 μ g) from all the cultured cells and poly A⁺RNA (1 μ g) from human brain (Clontech) was converted to cDNA by treatment with 200 units of MMLV reverse transcriptase (Bethesda Research Labs, MD) in 50 mM Tris-HCl, pH, 8.0, 1 mM dithiothreitol, 15 mM NaCl, 3 mM MgCl₂, 1 unit RNasin (Promega), 0.2 μ g of random hexamer primers, 0.8 mM dNTPs and incubated for 1 hour at 37° C. The reaction was terminated by heating at 95° C for 10 minutes and diluted to 1 ml with distilled water.

Enzymatic amplification was done on a 10 μ l aliquot of the cDNA mix. PCR was performed in 50 mM Tris-HCl, pH, 8.0, 1.5 mM MgCl₂, 10 mM KCl, 0.2 mM dNTPs, 0.5 μ g each of primers for edg-1 and 2.5 units of Taq DNA polymerase (Cetus, CA) (see, Saiki et al. (1988) Science 239, 487-491). The reaction mixture was heated at 94° C for 1 minute, annealed at 55° C for 2 minutes, and extended at 72° C for 3 minutes for 30 repetitive cycles. The primers used were as follows:

(1) 5'-TG TAC TGC AGA ATC TAC T-3' (sense) and 5'-T GCA GCC CAC ATC CAG CAG CA-3' (antisense) to amplify from nucleotide no. 909 to 1094, which spans the third cytosolic domain; and

(2) 5' AAG ACC TGT CAC ATC CTC TTC-3' (sense) and 5' ATG AAC CCT TTA GGA GCT TGA CAA-3' (antisense) to amplify from nucleotide no. 1100 to 1702, which spans the seventh transmembrane domain, the cytosolic tail and part of the 3'untranslated region.

1 When RNA from the various cultured human cell lines and
2 from human brain was reverse transcribed and the cDNAs
3 amplified using the oligonucleotides that are specific for the
4 C-terminal domain (amino acids 266 to the termination codon
5 and 309 bp of the 3' untranslated region, nucleotides 1100 to
6 1702, see, e.g., Figures 5-7 and 9) an amplified product is
7 the expected size, 600 bp., is observed (see Fig. 9 (A)) in
8 RNA from all cell types and human brain. The intensity of the
9 signal was most prominent in endothelial cells, but was
10 present to a lesser extent in smooth muscle cells,
11 fibroblasts, epidermoid cells, melanocytes, and brain tissue.

12 When the cDNAs were amplified with a pair of
13 oligonucleotides that span the third intracellular loop (amino
14 acids 220-282, nucleotides 909-1094), cell-specific bands were
15 amplified (Figure 9 (B)). In smooth muscle cells, a major
16 band at 0.7 Kb and minor bands at 0.9, 0.3, and 0.19 Kb were
17 observed. In HeLa cells a very prominent band was observed
18 at 0.3 Kb. The expected 0.19Kb amplification product was
19 observed only in endothelial cells.

20 This result indicates that cDNAs derived from mRNAs that
21 are related to, but not identical with, the *edg-1* transcript
22 are present in different cell types and tissues. Because the
23 third cytosolic loop has been identified in other G-protein-
24 coupled receptors as the region that binds to the G-protein,
25 the tissue specific transcripts differ in the region that
26 encodes the portion of the receptor that couples with the G-
27 protein and thereby modulates the cellular response of the
28 particular cell type to the specific signal.

29 Since modifications will be apparent to those of skill
30 in the art, it is intended that this invention be limited only
31 by the scope of the appended claims.

1 We claim:

2 1. A purified DNA molecule that encodes a protein having
3 the sequence of amino acids set forth in Figure 5.

4 2. The purified DNA molecule having the sequence of
5 nucleotide bases set forth in Figure 5.

6 3. A purified protein that has substantially the same
7 amino acid sequence as the sequence of amino acids set forth
8 in Figure 5.

9 4. A purified DNA molecule that encodes the protein of
10 claim 3.

11 5. A protein that includes regions that are
12 substantially homologous with all or a portion of the protein
13 of Figure 5, wherein said portion consists of the amino acids
14 that comprise the transmembrane domains of the protein of
15 Figure 5.

16 6. A protein selected from the group consisting of the
17 edg-1-G-coupled-protein receptor family of proteins.

18 7. The protein of claim 6, that is expressed in a cell
19 or tissue selected from the group consisting of smooth muscle
20 cells, fibroblasts, cultured immortal human cell lines,
21 epidermoid carcinoma cells, melanocytes, brain tissue and
22 differentiating endothelial cells.

23 8. An isolated DNA molecule that encodes the protein of
24 claim 7.

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FIG. 1

0 .5 1 2 4 hrs.
(A)



(B)



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FIG. 2

PMA	-	-	+	+	+
CHX	-	+	-	+	-
Act D	-	-	-	-	+

(A)



(B)



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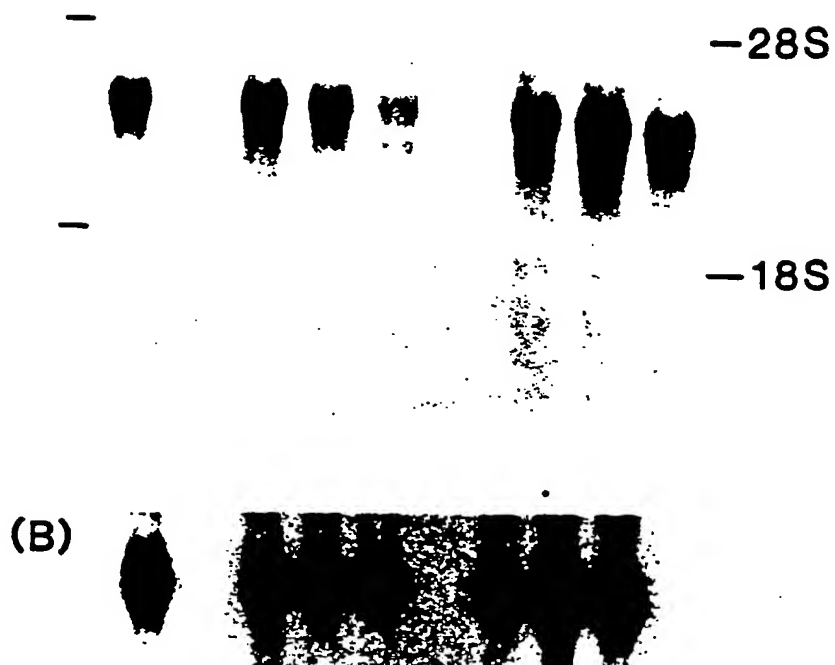
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FIG. 3

Act D	—	+	+	+	+	+	+
CHX	—	—	—	—	+	+	+
	0'	15'	30'	120'	15'	30'	120'

(A)

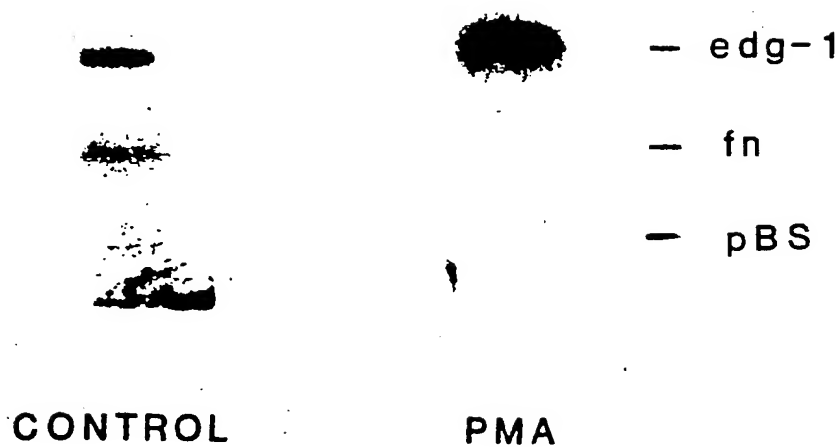


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FIG. 4



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10	20	30	40	50	60	70
TCTAAAGGTC	GGGGCAGCA	GCAAGATGCG	AAGCGAGCCG	TACAGATCCC	GGGCTCTCCG	AACGCAACTT
80	90	100	110	120	130	140
CGCCCTGCTT	GAGCGAGGCT	GCGGTTTCCG	AGGCCCTCTC	CAGCCAAGGA	AAAGCTACAC	AAAAAGCCTG
150	160	170	180	190	200	210
GATCACTCAT	CGAACCACCC	CTGAAGCCAG	TGAAGGCTCT	CTCGCCTCGC	CCTCTAGCGT	TCGTCTGGAG
220	230	240	250	259	268	
TAGCGCCACC	CCGGCTTCCT	GGGGACACAG	GGTTGGCACC	ATG GGG CCC	ACC AGC GTC	CCG
				MET	Gly	Pro
277	286	295	304	313	322	
CTG GTC AAG	GCC CAC	CGC AGC	TCG GTC	TCT GAC	TAT GAT	ATC
Leu Val Lys	Ala His	Arg Ser	Val Ser	Asp	Tyr Val	Asn
						Ile
331	340	349	358	367	376	
GTC CGG CAT	TAC AAC	TAC ACG	CTG AAT	ATC AGC	GAC AAG	GAG AAC
Val Arg His	Tyr Asn	Tyr Thr	Gly Lys	Leu Asn	Ile Ser	Ala Asp
						Lys Glu
385	394	403	412	421	430	
AGC ATT AAA	CTG ACC	TCG GTG	CTC ATT	CTC ATC	TGC TGC	TTT ATC
Ser Ile Lys	Leu Thr	Ser Val	Val Phe	Ile Leu	Cys Cys	Phe Ile
						Ile Leu
439	448	457	466	475	484	
GAG AAC ATC	TTT GTC	TTG CTG	ACC ATT	TGG AAA	ACC AAG	AAA TTC
Glu Asn Ile	Phe Val	Leu Thr	Ile Thr	Lys Lys	Thr Phe	His Arg
						Pro
493	502	511	520	529	538	
ATG TAC TAT	TTT ATT	GGC AAT	CTG GCC	CTC TCA	GAC CTG	TTG GCA
MET Tyr Tyr	Phe Ile	Gly Asn	Leu Ala	Leu Ser	Asp Leu	Leu Ala
						Gly Val
						Ala

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FIG. 5A

547	TAC ACA GCT AAC CTG CTC TTG TCT GGG GCC ACC ACC TAC AAG CTC ACT CCC GCC	556	565	574	583	592
Tyr Thr Ala Asn Leu Leu Leu Ser Gly Ala Thr Thr Tyr Lys Leu Thr Pro Ala						
601	CAG TGG TTT CTG CCG GAA GGG AGT ATG TTT GTG GCC CTG TCA GCC TCC GTG TTC	610	619	628	637	646
Gln Trp Phe Leu Arg Glu Gly Ser MET Phe Val Ala Leu Ser Ala Ser Val Phe						
655	AGT CTC CTC GCC ATC GCC ATT GAG CGC TAT ATC ACA ATG AAA ATG AAA CTC	664	673	682	691	700
Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr Ile Thr MET Leu Lys MET Lys Leu						
709	CAC AAC GGG AGC AAT AAC TTC CGC CTC TTC CTG CTA ATC AGC GCC TGC TGG GTC	718	727	736	745	754
His Asn Gly Ser Asn Asn Phe Arg Leu Phe Leu Leu Ile Ser Ala Cys Trp Val						
763	ATC TCC CTC ATC CTG GGT GGC CTG CCT ATC ATG GGC TGG AAC TGC ATC AGT GCG	772	781	790	799	808
Ile Ser Leu Ile Leu Gly Gly Leu Pro Ile MET Gly Trp Asn Cys Ile Ser Ala						
817	CTG TCC AGC TGC TCC ACC GTG CTG CCG CTC TAC CAC AAG CAC TAT ATC CTC TTC	826	835	844	853	862
Leu Ser Ser Cys Ser Thr Val Leu Leu Pro Leu Tyr His Lys His Tyr Ile Leu Phe						
871	TGC ACC ACG GTC TTC ACT CTG CTT CTG CTC TCC ATC GTC ATT CTG TAC TGC AGA	880	889	898	907	916
Cys Thr Thr Val Phe Thr Leu Leu Leu Ser Ile Val Ile Leu Tyr Cys Arg						

FIG. 5B

0

925	ATC TAC TCC TTG GTC	934	AGG ACT CGG AGC CGC CGC	943	CGG Arg Ser Arg Arg	952	CTG Leu Thr Phe	961	TTC Arg Lys Asn	970	ATT Ile
	Ile Tyr Ser Leu Val		Arg Thr Arg Ser Arg Arg		0						
979	TCC AAG GCC AGC CGC	988	AGC TCT GAG AAT GTG GCG	997	GAG Asn Val Ala	1006	CTG Leu Lys	1015	AAG ACC GTA ATT	1024	ATC Ser Lys Ala Ser Arg Ser
	0		0		0						
1033	GTC CTG AGC GTC TTC	1042	ATC GCC TGC TGG GCA CCG	1051	TGC TGG GCA CCG	1060	CTC TTC ATC	1069	CTG CTC CTG	1078	CTG Val Leu Ser Val Phe
	Ile Phe Val		Ile Ala Cys Trp Ala Pro		Leu Phe Ile		Leu Leu Leu		Leu Leu		Leu
1087	GAT GTG GGC TGC AAG	1096	GTG AAG ACC TGT GAC ATC	1105	TGT GAC ATC	1114	CTC TTC AGA	1123	GCG GAG TAC	1132	TTC Asp Val Gly Cys Lys
	Val Gly Cys Lys		Val Lys Thr Cys Asp Ile		Leu Phe Arg Ala Glu Tyr		Phe		Tyr		Phe
1141	CTG GTG TTA GCT GTG	1150	CTC AAC TCC GGC ACC AAC	1159	CCC ATC ATT	1168	TAC ACT CTG	1177	ACC	1186	Leu Val Leu Ala Val
	Leu Val Leu Ala Val		Leu Asn Ser Gly Thr Asn Pro		Ile Ile Tyr Thr Leu		Thr		Thr		Thr
1195	AAC AAG GAG ATG CGT	1204	CGG GCC TTC ATC CGG ATC	1213	ATG TCC TGC	1222	TGC AAG TGC	1231	CCG	1240	Pro
	Asn Lys Glu MET Arg		Arg Ala Phe Ile Arg Ile		MET Ser Cys		Lys Cys		Pro		
1249	ACC GGA GAC TCT GCT	1258	GGC AAA TTC AAG CGA CCC	1267	ATC ATC GCC	1276	GGC ATG GAA	1285	TTC	1294	Phe
	Ser Gly Asp Ser Ala		Gly Lys Phe Lys Arg Pro		Ile Ile Ala		Gly MET Glu		Phe		

FIG. 5C

1303 1312 1321 1330 1339 1348
 AGC CGC AGC AAA TCG GAC AAT TCC TCC CAC CCC CAG AAA GAC GAA GGG GAC AAC
 Ser Arg Ser Lys Ser Asp Asn Ser Ser Ser His Pro Gln Lys Asp Glu Gly Asp Asn 0/13

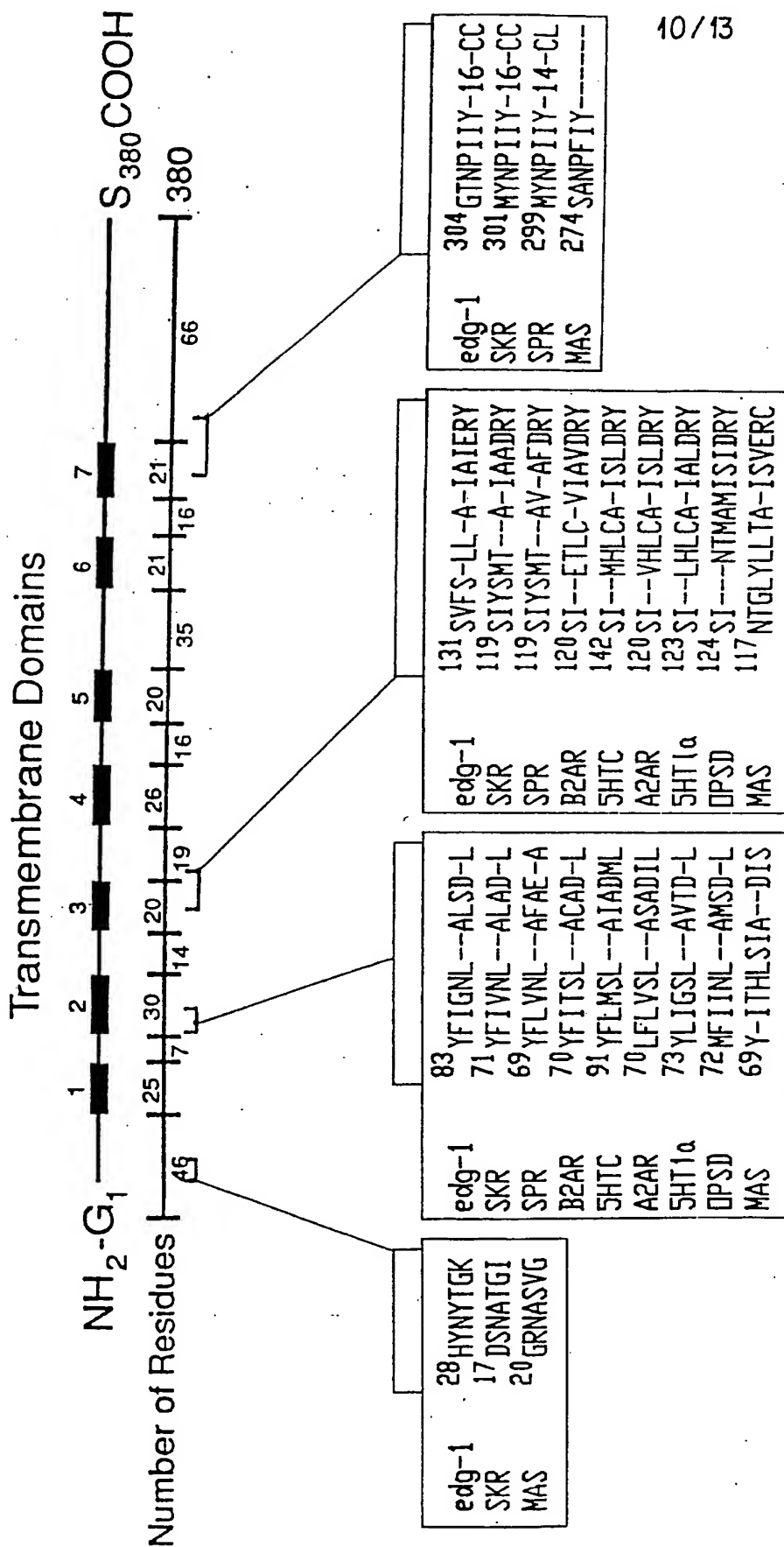
 1357 1366 1375 1384 1393 1406
 CCA GAG ACC ATT ATG TCT TCT GGA AAC GTC AAC TCT TCT TCC TAG AACTGGAAGC
 Pro Glu Thr Ile MET Ser Ser Ser Gly Asn Val Asn Ser Ser Ser
 1416 1426 1436 1446 1456 1466 1476
 TGTCCACCCA CCGGAAGCGC TCTTTACTTG GTCGCTGGCC ACCCCAGTGT TTGGAAAAA ATCTCTGGGC
 1486 1496 1506 1516 1526 1536 1546
 TTCGACTGCT GCCAGGGAGG AGCTGCTGCA AGCCAGAGGG AGGAAGGGG AGAATACGAA CAGCCTGGTG
 1556 1566 1576 1586 1596 1606 1616
 GTGTCGGGTG TTGGTGGTA GAGTTAGTTC CTGTGAACAA TGCACCTGGGA AGGGTGGAGA TCAGGTCCCCG
 1626 1636 1646 1656 1666 1676 1686
 GCCTGGAATA TATATTCTAC CCCCCTGGAG CTTTGATTTT GCACTGAGCC AAAGTCTAG CATTGTCAAG
 1696 1706 1716 1726 1736 1746 1756
 CTCCTAAAGG GTTCATTGG CCCCCTCCTCA AAGACTAATG TCCCCATGTG AAAGCGTCTC TTTGTCTGGA
 1766 1776 1786 1796 1806 1816 1826
 GCTTTGAGGA GATGTTTCC TTCACCTTAG TTTCAAACCC AAGTGAGTGT GTGCACTTCT GCTTCTTTAG
 1836 1846 1856 1866 1876 1886 1896
 GGATGCCCTG TACATCCCAC ACCCCACCCT CCGTTCCCTT CATACCCCTC CTCACGTTT TTTTACTTTA
 1906 1916 1926 1936 1946 1956 1966
 TACTTTAACT ACCTGAGAGT TATCAGAGCT GGGGTTGTGG AATGATCGAT CATCTATAGC AAATAGGCTA
 1976 1986 1996 2006 2016 2026 2036
 TGTGAGTAC GTAGGCTGTG GGAAGATGAA GATGTTTGG AGGTGTAAAA CAATGTCCTT CGCTGAGGCC

FIG. 5D

2046	2056	2066	2076	2086	2096	2106
AAAGTTTCCA	TGTAAGCGGG	ATCCGTTTTT	TGGAATTTGG	TTGAAGTCAC	TTTGATTTCT	TTAAAAACA
2116	2126	2136	2146	2156	2166	2176
TCTTTTCAAT	GAAATGTGTT	ACCATTTTCA	ATCCATTGAA	GCCGAAATCT	GCATAAGGAA	GCCCACTTTA
2186	2196	2206	2216	2226	2236	2246
TCTAAATGAT	ATTAGCCAGG	ATCCTTGGTG	TCCTAGGAGA	AACAGACAAG	CAAAACAAAG	TGAAAAACCGA
2256	2266	2276	2286	2296	2306	2316
ATGGATTAC	TTTTGCAAC	CAAGGAGAT	TTCTTAGCAA	ATGAGTCTAA	CAAATATGAC	ATCCGTCCTT
2326	2336	2346	2356	2366	2376	2386
CCCACTTTTG	TTGATGTTTA	TTTCAGAATC	TTGTGTGATT	CATTTCAGC	AACAACATGT	TGTATTTTGT
2396	2406	2416	2426	2436	2446	2456
TGTGTTAAAA	GTAATTTTCT	TGATTTTGA	ATGTATTTGT	TTCAGGAAGA	AGTCATTTTA	TGGATTTTTC
2466	2476	2486	2496	2506	2516	2526
TAACCCGTGT	TAACTTTTCT	AGAATCCACC	CTCTTGTC	CTTAAGCATT	ACTTTAACTG	GTAGGGAACG
2536	2546	2556	2566	2576	2586	2596
CCAGAACTTT	TAAAGTCCAGC	TATTCATTAG	ATAGTAATTG	AAGATATGTA	TAAATATTAC	AAAGAATAAAA
2606	2616	2626	2636	2646	2656	2666
AATATATTAC	TGTCTCTTTA	GTATGGTTTT	CAGTGCAATT	AAACCGAGAG	ATGCTCTGTT	TTTTTAAAAA
2676	2686	2696	2706	2716	2726	2736
GAATAGTATT	TAATAGGTTT	CTGACTTTTG	TGGATCATT	TGCACATAGC	TTTATCAACT	TTTAAACATT
2746	2756	2766				
AAATAAACTGA	TTTTTTTAAA	GAAAAAATAA	AAAAAAAG			
=====						

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FIG. 5E



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FIG. 6

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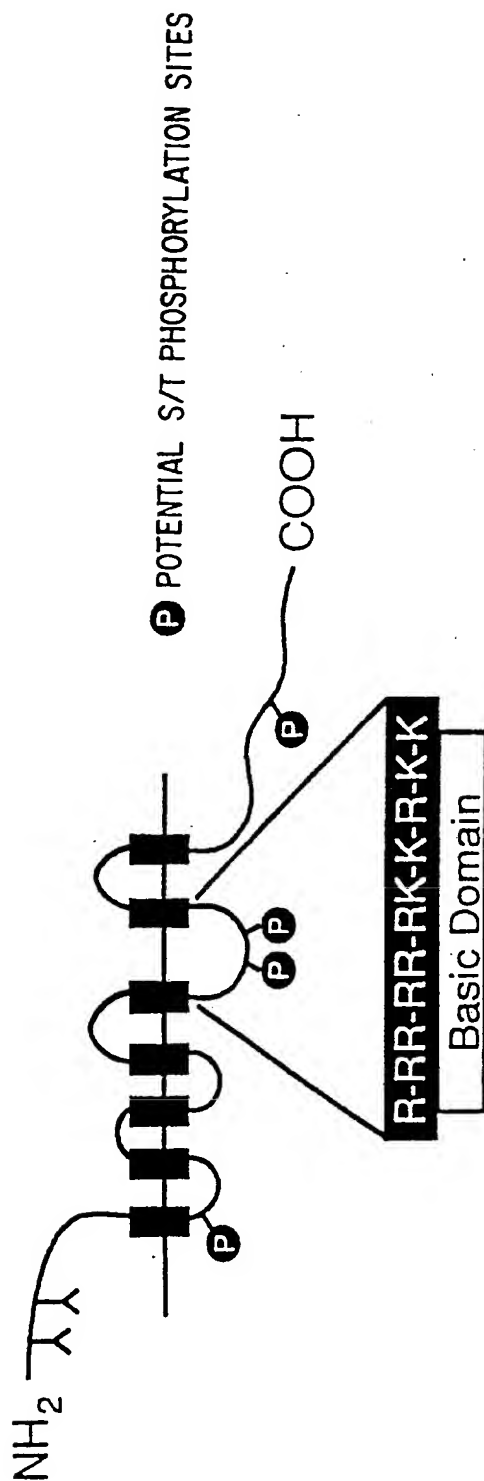


FIG. 7

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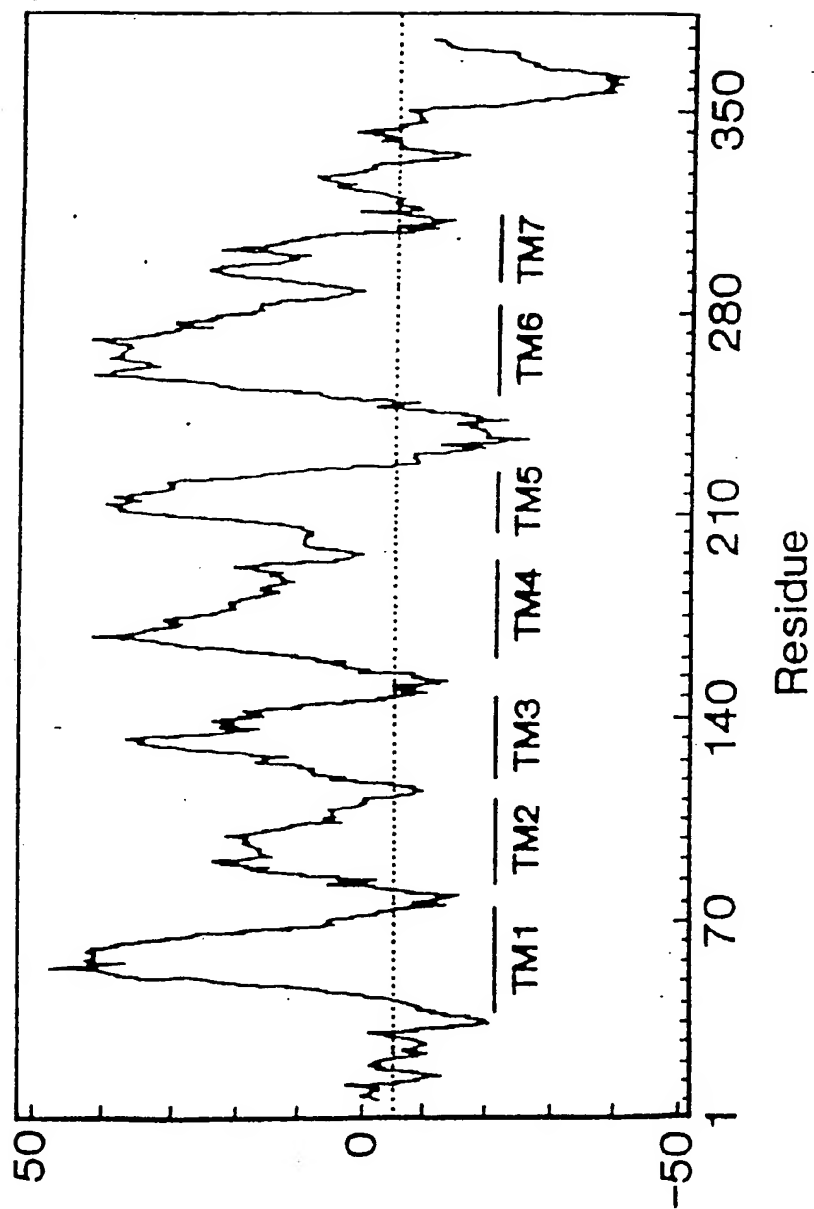


FIG. 8

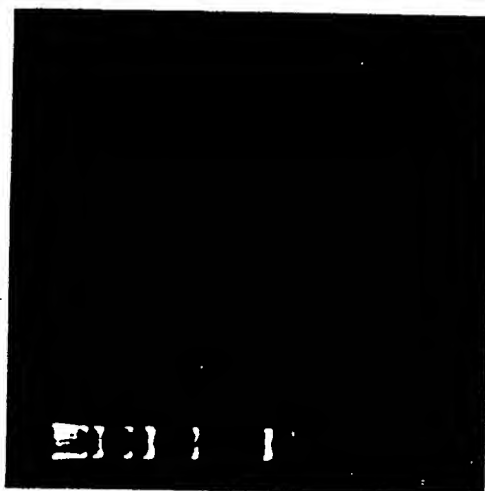
Hydropobicity

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FIG. 9B

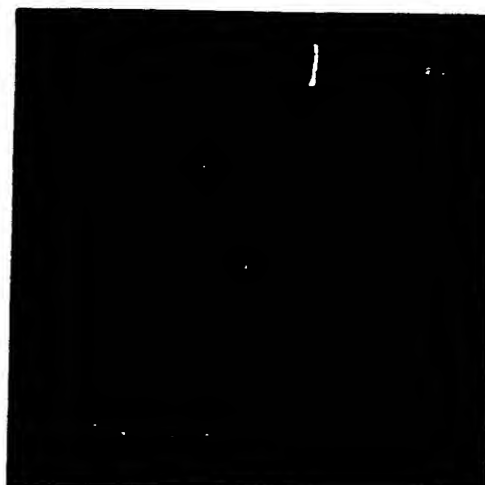
S F A H M B E



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FIG. 9A

S F A H M B E



▲ ▲ ▲ ▲ ▲

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INTERNATIONAL SEARCH REPORT

International Application No. PCT/US91/02344

I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all *) According to International Patent Classification (IPC) or to both National Classification and IPC IPC(5): C12N 15/12; C07K 15/06; 15/14 U.S.CL.: 536/27, 530/350,395		
II. FIELDS SEARCHED		
Minimum Documentation Searched *		
Classification System	Classification Symbols	
U.S.C1.	536/27; 530/350,395.	
Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched *		
APS AND DIALOG Files 357,155,WPI,72,35,5 and 399 searched for edg type receptor proteins and sequences.		
III. DOCUMENTS CONSIDERED TO BE RELEVANT *		
Category *	Citation of Document, ** with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
X,P	Journal of Biological Chemistry, vol. 265, No. 16, issued 05 June 1990. Hla et al., "An abundant transcript induced in differentiating human endothelial cells encodes a polypeptide with structural similarities to G-protein- coupled receptors", pages 9308-9313. See whole publication, especially the abstract, p. 9309 and 9311.	1-8
X	Science, vol. 241, issued 16 September 1988. Klein et al., "A chemoattractant receptor controls development in <u>Dictyostelium</u> <u>discoideum</u> ", pages 1467-1472. See whole publications, especially Figure 8 on p. 1472.	3-8
A	Science, vol. 245, issued 08 September 1989; Devreotes. " <u>Dictyostelium discoideum</u> : a model system for cell-cell interactions in development", pages 1054-1058. See whole publication.	1-8
<p>* Special categories of cited documents: ¹⁰</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claims) or which is cited to establish the publication date of another citation or other special reason (its specification)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> <p>"I" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is considered with one or more other such docu- ments, such combination being obvious to a person skilled in the art</p> <p>Δ* document member of the same patent family</p>		
IV. CERTIFICATION		
Date of the Actual Completion of the International Search		Date of Mailing of the International Search Report
02 July 1991		26 JUL 1991
International Searching Authority		Keith C. Furman
ISA/US		KEITH C. FURMAN